



## SEQUENCE LISTING

<110> ARCANGEL, Phillip  
CHIEN, David Y.

<120> HCV ASSAY

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<150> 60/409,515  
<151> 2002-09-09

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<170> PatentIn version 3.2

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Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly  
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gag gtc cag att gtg tca act gct gcc caa acc ttc ctg gca acg tgc 144  
Glu Val Gln Ile Val Ser Thr Ala Ala Gln Thr Phe Leu Ala Thr Cys  
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Ile Ala Ser Pro Lys Gly Pro Val Ile Gln Met Tyr Thr Asn Val Asp  
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Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu  
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595 600 605	
gaa atc acc ctg acg cac cca gtc acc aaa tac atc atg aca tgc atg	1872
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His Ile Thr Gly His Arg Met Ala Trp Lys Leu Gly Ser Ala Ala Arg	
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Thr Thr Ser Gly Phe Val Ser Leu Phe Ala Pro Gly Ala Lys Gln Asn	
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Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser	
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Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr	
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 His Glu Phe Gly Asp Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His  
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 His Ile Thr Gly His Arg Met Ala Trp Lys Leu Gly Ser Ala Ala Arg  
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 Ser Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val  
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 Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro  
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Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser  
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Ala Glu Met Leu Lys Ser Lys Ile Gln Gly Leu Leu Gly Ile Leu Arg  
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 Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro  
 820 825

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<211> 3297  
 <212> DNA  
 <213> Artificial

<220>  
 <223> MEFA 7.1 DNA sequence

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 ggt att att aac ttc gag cag aag gaa agt aat gga cca gtg aag gtg 96  
 Gly Ile Ile Asn Phe Glu Gln Lys Glu Ser Asn Gly Pro Val Lys Val  
 20 25 30  
 tgg gga agc att aaa gga ctg act gaa ggc ctg cat gga ttc cat gtt 144  
 Trp Gly Ser Ile Lys Gly Leu Thr Glu Gly Leu His Gly Phe His Val  
 35 40 45  
 cat gag ttt gga gat aat aca gca ggc tgt acc agt gca ggt cct cac 192  
 His Glu Phe Gly Asp Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His  
 50 55 60  
 ttt aat cct cta tcc aga aaa cac ggt ggg cca aag gat gaa gag agg 240  
 Phe Asn Pro Leu Ser Arg Lys His Gly Gly Pro Lys Asp Glu Glu Arg  
 65 70 75 80  
 cat gtt gga gac ttg ggc aat gtg act gct gac aaa gat ggt gtg gcc 288  
 His Val Gly Asp Leu Gly Asn Val Thr Ala Asp Lys Asp Gly Val Ala  
 85 90 95  
 gat gtg tct att gaa gat tct gtg atc tca ctc tca gga gac cat tgc 336  
 Asp Val Ser Ile Glu Asp Ser Val Ile Ser Leu Ser Gly Asp His Cys  
 100 105 110  
 atc att ggc cgc aca ctg gtg gtc cat gaa aaa gca gat gac ttg ggc 384  
 Ile Ile Gly Arg Thr Leu Val Val His Glu Lys Ala Asp Asp Leu Gly  
 115 120 125  
 aaa ggt gga aat gaa gaa agt aca aag aca gga aac gct gga agt cgt 432  
 Lys Gly Gly Asn Glu Glu Ser Thr Lys Thr Gly Asn Ala Gly Ser Arg  
 130 135 140  
 ttg gct tgt ggt gta att ggg atc gcc cag aat ttg aat tct ggt tgc 480  
 Leu Ala Cys Gly Val Ile Gly Ile Ala Gln Asn Leu Asn Ser Gly Cys  
 145 150 155 160  
 aat tgc tct atc tat ccc ggc cat ata acg ggt cac cgc atg gca tgg 528  
 Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp  
 165 170 175  
 aag ctt ggt tcc gcc gcc aga act acc tcg ggc ttt gtc tcc ttg ttc 576  
 Lys Leu Gly Ser Ala Ala Arg Thr Thr Ser Gly Phe Val Ser Leu Phe  
 180 185 190  
 gcc cca ggt gcc aaa caa aac gaa act cac gtc acg gga ggc gca gcc 624  
 Ala Pro Gly Ala Lys Gln Asn Glu Thr His Val Thr Gly Gly Ala Ala  
 195 200 205

gcc cga act acg tct ggg ttg acc tct ttg ttc tcc cca ggt gcc agc	672
Ala Arg Thr Thr Ser Gly Leu Thr Ser Leu Phe Ser Pro Gly Ala Ser	
210 215 220	
caa aac att caa ttg att gtc gac ttt atc cct gtg gag aac cta gag	720
Gln Asn Ile Gln Leu Ile Val Asp Phe Ile Pro Val Glu Asn Leu Glu	
225 230 235 240	
aca acc atg cga tct ccg gtg ttc acg gat aac tcc tct cca cca gta	768
Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Val	
245 250 255	
gtg ccc cag agc ttc cag gtg gct cac ctc cat gct ccc aca ggc agc	816
Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser	
260 265 270	
ggc aaa agc acc aag gtc ccg gct gca tat gca gct cag ggc tat aag	864
Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys	
275 280 285	
gtg cta gta ctc aac ccc tct gtt gct gca aca ctg ggc ttt ggt gct	912
Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala	
290 295 300	
tac atg tcc aag gct cat ggg atc gat cct aac atc agg acc ggg gtg	960
Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val	
305 310 315 320	
aga aca att acc act ggc agc ccc atc acg tac tcc acc tac ggc aag	1008
Arg Thr Ile Thr Thr Gly Ser Pro Ile Thr Tyr Ser Thr Tyr Gly Lys	
325 330 335	
ttc ctt gcc gac ggc ggg tgc tcg ggg ggc gct tat gac ata ata att	1056
Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile	
340 345 350	
tgt gac gag tgc cac tcc acg gat gcc aca tcc atc ttg ggc att ggc	1104
Cys Asp Glu Cys His Ser Thr Asp Ala Thr Ser Ile Leu Gly Ile Gly	
355 360 365	
act gtc ctt gac caa gca gag act gcg ggg gcg aga ctg gtt gtg ctc	1152
Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu	
370 375 380	
gcc acc gcc acc cct ccg ggc tcc gtc act gtg ccc cat ccc aac atc	1200
Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile	
385 390 395 400	
gag gag gtt gct ctg tcc acc acc gga gag atc cct ttt tac ggc aag	1248
Glu Glu Val Ala Leu Ser Thr Thr Gly Glu Ile Pro Phe Tyr Gly Lys	
405 410 415	
gct atc ccc ctc gaa gta atc aag ggg ggg aga cat ctc atc ttc tgt	1296
Ala Ile Pro Leu Glu Val Ile Lys Gly Gly Arg His Leu Ile Phe Cys	
420 425 430	
cat tca aag aag aag tgc gac gaa ctc gcc gca aag ctg gtc gca ttg	1344
His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Val Ala Leu	
435 440 445	

ggc atc aat gcc gtg gcc tac tac cgc ggt ctt gac gtg tcc gtc atc	1392
Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile	
450 455 460	
ccg acc agc ggc gat gtt gtc gtc gtg gca acc gat gcc ctc atg acc	1440
Pro Thr Ser Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met Thr	
465 470 475 480	
ggc tat acc ggc gac ttc gac tcg gtg ata gac tgc aat acg tgt gtc	1488
Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val	
485 490 495	
acc cag aca gtc gat ttc agc ctt gac cct acc ttc acc att gag aca	1536
Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr	
500 505 510	
atc acg ctc ccc caa gat gct gtc tcc cgc act caa cgt cgg ggc agg	1584
Ile Thr Leu Pro Gln Asp Ala Val Ser Arg Thr Gln Arg Arg Gly Arg	
515 520 525	
act ggc agg ggg aag cca ggc atc tac aga ttt gtg gca ccg ggg gag	1632
Thr Gly Arg Gly Lys Pro Gly Ile Tyr Arg Phe Val Ala Pro Gly Glu	
530 535 540	
cgc ccc tcc ggc atg ttc gac tcg tcc gtc ctc tgt gag tgc tat gac	1680
Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp	
545 550 555 560	
gca ggc tgt gct tgg tat gag ctc acg ccc gcc gag act aca gtt agg	1728
Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Thr Val Arg	
565 570 575	
cta cga gcg tac atg aac acc ccg ggg ctt ccc gtg tgc cag gac cat	1776
Leu Arg Ala Tyr Met Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His	
580 585 590	
ctt gaa ttt tgg gag ggc gtc ttt aca ggc ctc act cat ata gat gcc	1824
Leu Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr His Ile Asp Ala	
595 600 605	
cac ttt cta tcc cag aca aag cag agt ggg gag aac ctt cct tac ctg	1872
His Phe Leu Ser Gln Thr Lys Gln Ser Gly Glu Asn Leu Pro Tyr Leu	
610 615 620	
gta gcg tac caa gcc acc gtg tgc gct agg gct caa gcc cct ccc cca	1920
Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro	
625 630 635 640	
tcg tgg gac cag atg tgg aag tgt ttg att cgc ctc aag ccc acc ctc	1968
Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu	
645 650 655	
cat ggg cca aca ccc ctg cta tac aga ctg ggc gct gtt cag aat gaa	2016
His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu	
660 665 670	
atc acc ctg acg cac cca gtc acc aaa tac atc atg aca tgc atg tcg	2064
Ile Thr Leu Thr His Pro Val Thr Lys Tyr Ile Met Thr Cys Met Ser	
675 680 685	

gcc gac ctg gag gtc gtc acg agc gca tgc tcc ggg aag ccg gca atc Ala Asp Leu Glu Val Val Thr Ser Ala Cys Ser Gly Lys Pro Ala Ile 690 695 700	2112
ata cct gac agg gaa gtc ctc tac cga gag ttc gat gag atg gaa gag Ile Pro Asp Arg Glu Val Leu Tyr Arg Glu Phe Asp Glu Met Glu Glu 705 710 715 720	2160
tgc tct cag cac tta ccg tac atc gag caa ggg atg atg ctc gcc gag Cys Ser Gln His Leu Pro Tyr Ile Glu Gln Gly Met Met Leu Ala Glu 725 730 735	2208
cag ttc aag cag aag gcc ctc ggc ctc tcg cga ggg ggc aag ccg gca Gln Phe Lys Gln Lys Ala Leu Gly Leu Ser Arg Gly Gly Lys Pro Ala 740 745 750	2256
atc gtt cca gac aaa gag gtg ttg tat caa caa tac gat gag atg gaa Ile Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu 755 760 765	2304
gag tgc tca caa gct gcc cca tat atc gaa caa gct cag gta ata gct Glu Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala 770 775 780	2352
cac cag ttc aag gaa aaa gtc ctt gga ttg atc gat aat gat caa gtg His Gln Phe Lys Glu Lys Val Leu Gly Leu Ile Asp Asn Asp Gln Val 785 790 795 800	2400
gtt gtg act cct gac aaa gaa atc tta tat gag gcc ttt gat gag atg Val Val Thr Pro Asp Lys Glu Ile Leu Tyr Glu Ala Phe Asp Glu Met 805 810 815	2448
gaa gaa tgc gcc tcc aaa gcc gcc ctc att gag gaa ggg cag cgg atg Glu Glu Cys Ala Ser Lys Ala Ala Leu Ile Glu Glu Gly Gln Arg Met 820 825 830	2496
gcg gag atg ctc aag tct aag ata caa ggc ctc ctc ggg ata ctg cgc Ala Glu Met Leu Lys Ser Lys Ile Gln Gly Leu Leu Gly Ile Leu Arg 835 840 845	2544
cgg cac gtt ggt cct ggc gag ggg gca gtg cag tgg atg aac cgg ctg Arg His Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu 850 855 860	2592
ata gcc ttc gcc tcc aga ggg aac cat gtt tcc ccc acg cac tac gtt Ile Ala Phe Ala Ser Arg Gly Asn His Val Ser Pro Thr His Tyr Val 865 870 875 880	2640
ccg tct aga tcc cgg aga ttc gcc cag gcc ctg ccc gtt tgg gcg cgg Pro Ser Arg Ser Arg Arg Phe Ala Gln Ala Leu Pro Val Trp Ala Arg 885 890 895	2688
ccg gac tat aac ccc ccg cta gtg gag acg tgg aaa aag ccc gac tac Pro Asp Tyr Asn Pro Pro Leu Val Glu Thr Trp Lys Lys Pro Asp Tyr 900 905 910	2736
gaa cca cct gtg gtc cac ggc aga tct tct cgg aga ttc gcc cag gcc Glu Pro Pro Val Val His Gly Arg Ser Ser Arg Arg Phe Ala Gln Ala 915 920 925	2784



ctg ccc gtt tgg gcg cgg ccg gac tat aac ccc ccg cta gtg gag acg 2832  
 Leu Pro Val Trp Ala Arg Pro Asp Tyr Asn Pro Pro Leu Val Glu Thr  
 930 935 940

tgg aaa aag ccc gac tac gaa cca cct gtg gtc cat ggc aga aag acc 2880  
 Trp Lys Lys Pro Asp Tyr Glu Pro Pro Val Val His Gly Arg Lys Thr  
 945 950 955 960

aaa cgt aac acc aac cgg cgg ccg cag gac gtc aag ttc ccg ggt ggc 2928  
 Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly  
 965 970 975

ggt cag atc gtt ggt cgc agg ggc cct cct atc ccc aag gct cgt cgg 2976  
 Gly Gln Ile Val Gly Arg Arg Gly Pro Pro Ile Pro Lys Ala Arg Arg  
 980 985 990

ccc gag ggc agg acc tgg gct cag ccc ggt tac cct tgg ccc ctc tat 3024  
 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr  
 995 1000 1005

ggc aat aag gac aga cgg tct aca ggt aag tcc tgg ggt aag cca ggg 3072  
 Gly Asn Lys Asp Arg Arg Thr Gly Lys Ser Trp Gly Lys Pro Gly  
 1010 1015 1020

tac cct tgg cca aga aag acc aaa cgt aac acc aac cga cgg ccg cag 3120  
 Tyr Pro Trp Pro Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln  
 1025 1030 1035 1040

gac gtc aag ttc ccg ggt ggc ggt cag atc gtt ggt cgc agg ggc cct 3168  
 Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Arg Arg Gly Pro  
 1045 1050 1055

cct atc ccc aag gct cgt cgg ccc gag ggc agg acc tgg gct cag ccc 3216  
 Pro Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro  
 1060 1065 1070

ggt tac cct tgg ccc ctc tat ggc aat aag gac aga cgg tct acc ggt 3264  
 Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Lys Asp Arg Arg Ser Thr Gly  
 1075 1080 1085

aag tcc tgg ggt aag cca ggg tat cct tgg ccc 3297  
 Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro  
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 <212> PRT  
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<220>  
 <223> MEFA 7.1 amino acid sequence

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Trp Gly Ser Ile Lys Gly Leu Thr Glu Gly Leu His Gly Phe His Val  
 35 40 45  
 His Glu Phe Gly Asp Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His  
 50 55 60  
 Phe Asn Pro Leu Ser Arg Lys His Gly Gly Pro Lys Asp Glu Glu Arg  
 65 70 75 80  
 His Val Gly Asp Leu Gly Asn Val Thr Ala Asp Lys Asp Gly Val Ala  
 85 90 95  
 Asp Val Ser Ile Glu Asp Ser Val Ile Ser Leu Ser Gly Asp His Cys  
 100 105 110  
 Ile Ile Gly Arg Thr Leu Val Val His Glu Lys Ala Asp Asp Leu Gly  
 115 120 125  
 Lys Gly Gly Asn Glu Glu Ser Thr Lys Thr Gly Asn Ala Gly Ser Arg  
 130 135 140  
 Leu Ala Cys Gly Val Ile Gly Ile Ala Gln Asn Leu Asn Ser Gly Cys  
 145 150 155 160  
 Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp  
 165 170 175  
 Lys Leu Gly Ser Ala Ala Arg Thr Thr Ser Gly Phe Val Ser Leu Phe  
 180 185 190  
 Ala Pro Gly Ala Lys Gln Asn Glu Thr His Val Thr Gly Gly Ala Ala  
 195 200 205  
 Ala Arg Thr Thr Ser Gly Leu Thr Ser Leu Phe Ser Pro Gly Ala Ser  
 210 215 220  
 Gln Asn Ile Gln Leu Ile Val Asp Phe Ile Pro Val Glu Asn Leu Glu  
 225 230 235 240  
 Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Val  
 245 250 255  
 Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser  
 260 265 270  
 Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys  
 275 280 285  
 Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala  
 290 295 300

Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val  
 305 310 315 320  
 Arg Thr Ile Thr Thr Gly Ser Pro Ile Thr Tyr Ser Thr Tyr Gly Lys  
 325 330 335  
 Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile  
 340 345 350  
 Cys Asp Glu Cys His Ser Thr Asp Ala Thr Ser Ile Leu Gly Ile Gly  
 355 360 365  
 Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu  
 370 375 380  
 Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile  
 385 390 395 400  
 Glu Glu Val Ala Leu Ser Thr Thr Gly Glu Ile Pro Phe Tyr Gly Lys  
 405 410 415  
 Ala Ile Pro Leu Glu Val Ile Lys Gly Gly Arg His Leu Ile Phe Cys  
 420 425 430  
 His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Val Ala Leu  
 435 440 445  
 Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile  
 450 455 460  
 Pro Thr Ser Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met Thr  
 465 470 475 480  
 Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val  
 485 490 495  
 Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr  
 500 505 510  
 Ile Thr Leu Pro Gln Asp Ala Val Ser Arg Thr Gln Arg Arg Gly Arg  
 515 520 525  
 Thr Gly Arg Gly Lys Pro Gly Ile Tyr Arg Phe Val Ala Pro Gly Glu  
 530 535 540  
 Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp  
 545 550 555 560  
 Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Thr Val Arg  
 565 570 575  
 Leu Arg Ala Tyr Met Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His  
 580 585 590  
 Leu Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr His Ile Asp Ala  
 595 600 605



Glu Pro Pro Val Val His Gly Arg Ser Ser Arg Arg Phe Ala Gln Ala  
 915 920 925

Leu Pro Val Trp Ala Arg Pro Asp Tyr Asn Pro Pro Leu Val Glu Thr  
 930 935 940

Trp Lys Lys Pro Asp Tyr Glu Pro Pro Val Val His Gly Arg Lys Thr  
 945 950 955 960

Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly  
 965 970 975

Gly Gln Ile Val Gly Arg Arg Gly Pro Pro Ile Pro Lys Ala Arg Arg  
 980 985 990

Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr  
 995 1000 1005

Gly Asn Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly  
 1010 1015 1020

Tyr Pro Trp Pro Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln  
 1025 1030 1035 1040

Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Arg Arg Gly Pro  
 1045 1050 1055

Pro Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro  
 1060 1065 1070

Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Lys Asp Arg Arg Ser Thr Gly  
 1075 1080 1085

Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro  
 1090 1095

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 <211> 21  
 <212> PRT  
 <213> Artificial

<220>  
 <223> consensus sequence

<400> 7

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Gly Ala Lys Gln Asn  
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<220>

<223> sequence following HindIII site

<400> 8

acaaaacaaa

10

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<211> 23

<212> PRT

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<400> 9

Lys Lys Gly Ser Val Val Ile Val Gly Arg Ile Val Leu Ser Gly Lys  
1 5 10 15

Pro Ala Ile Ile Pro Lys Lys  
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